

FIG. 1A.

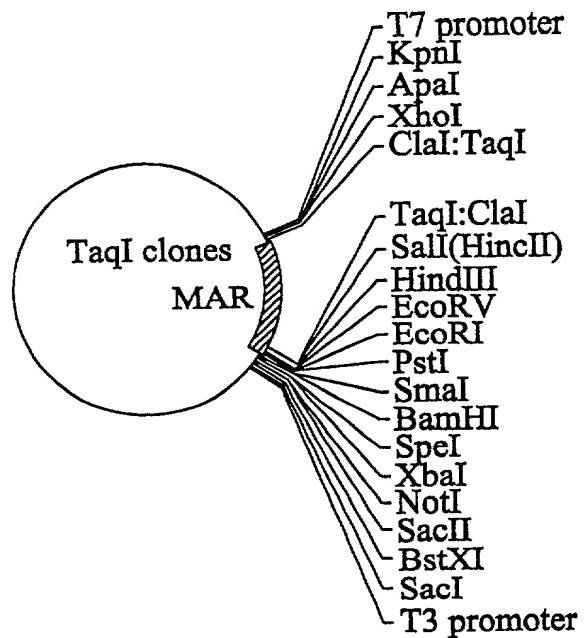


FIG. 1B.

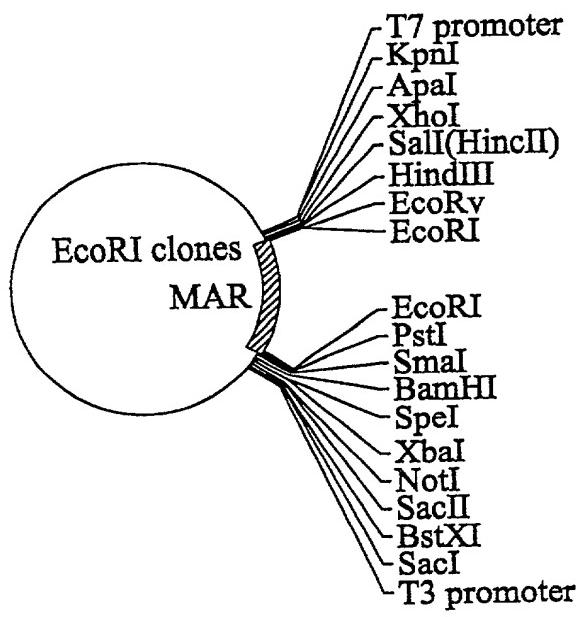


FIG. 1C.

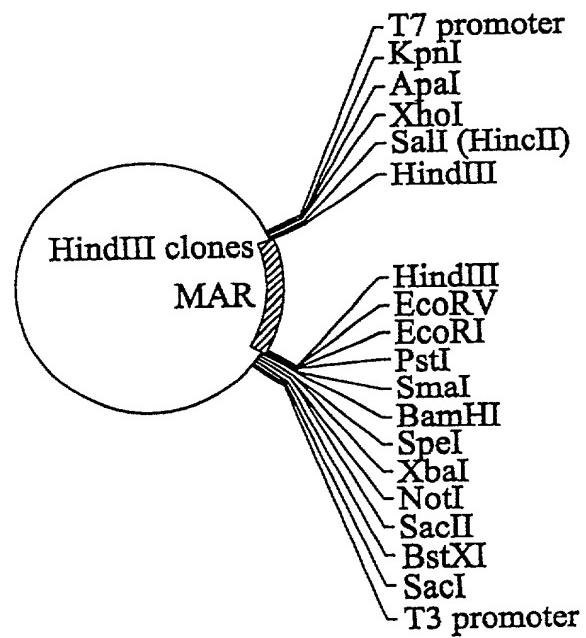
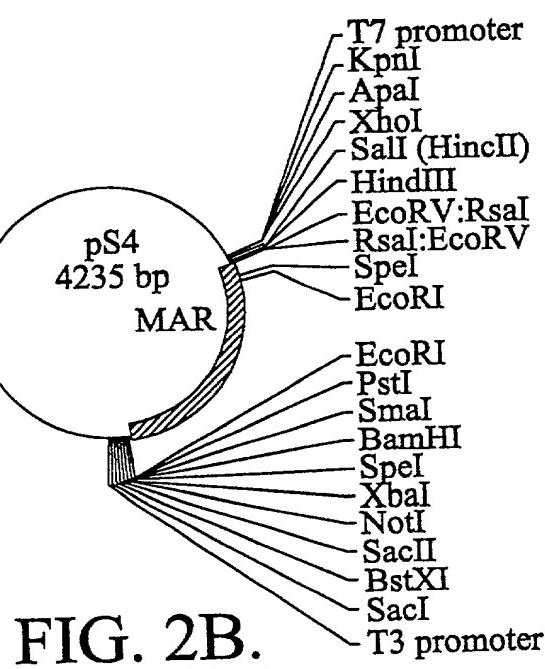
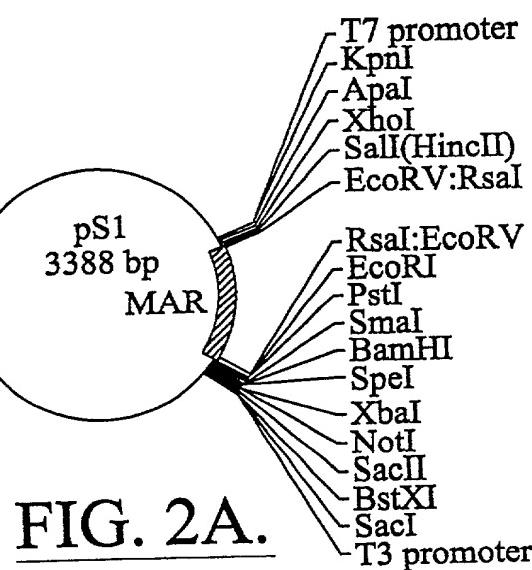
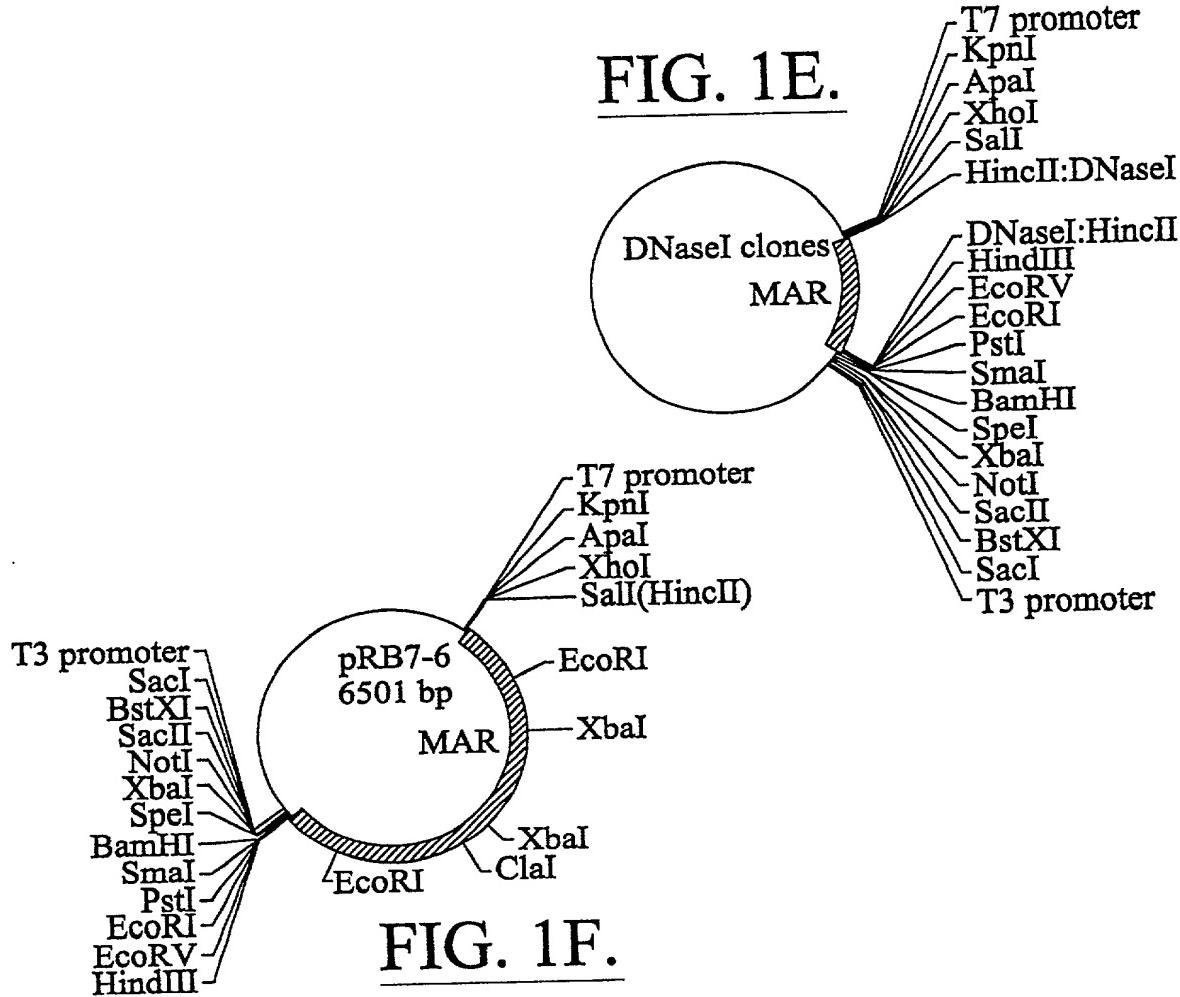


FIG. 1D.

FIG. 1E.



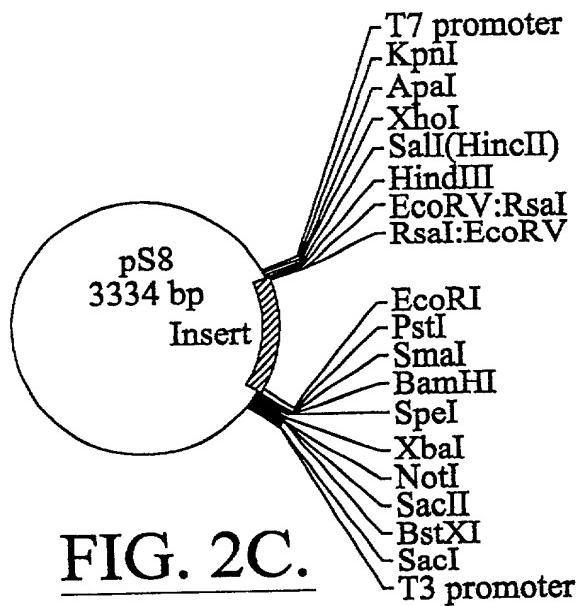


FIG. 2C.

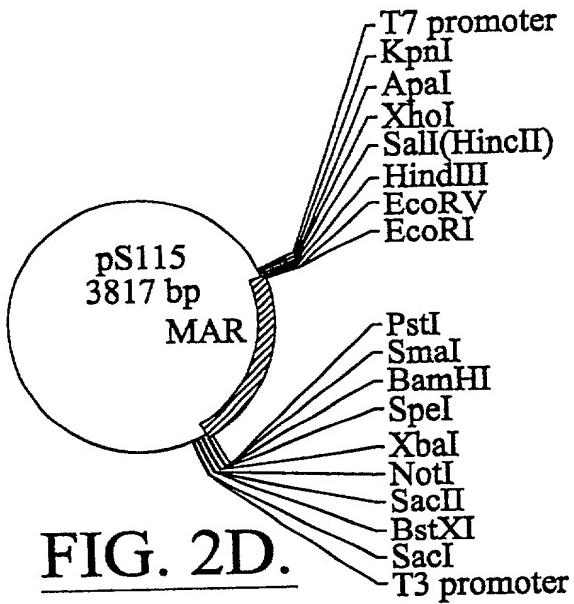


FIG. 2D.

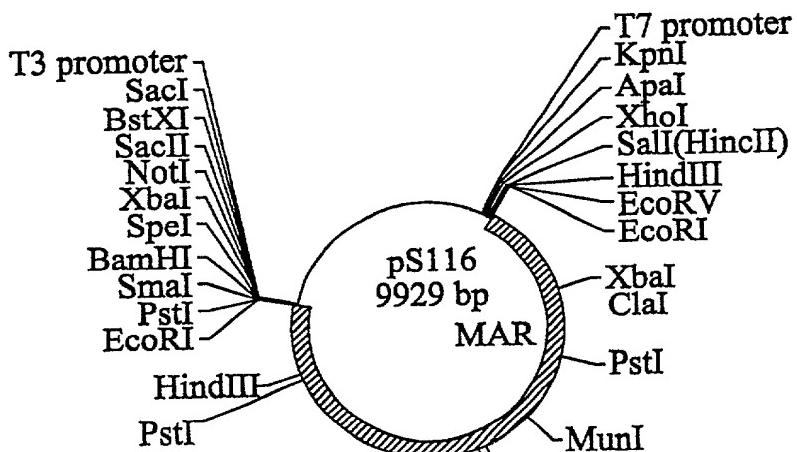


FIG. 2E.

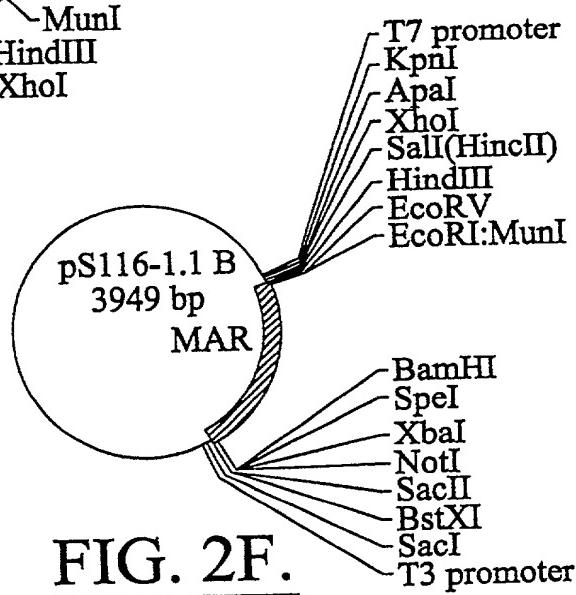


FIG. 2F.

FIG. 2G.

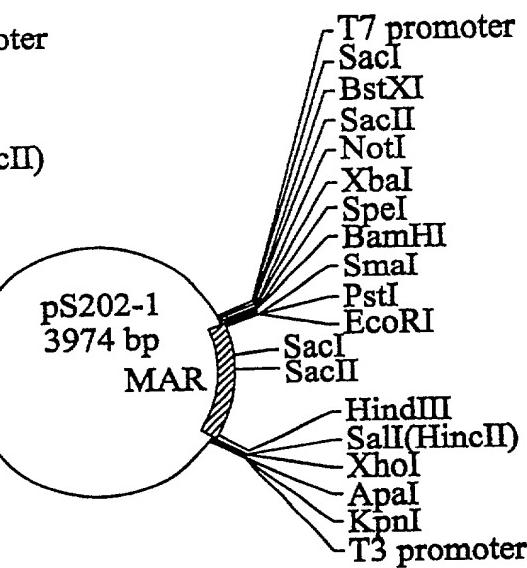
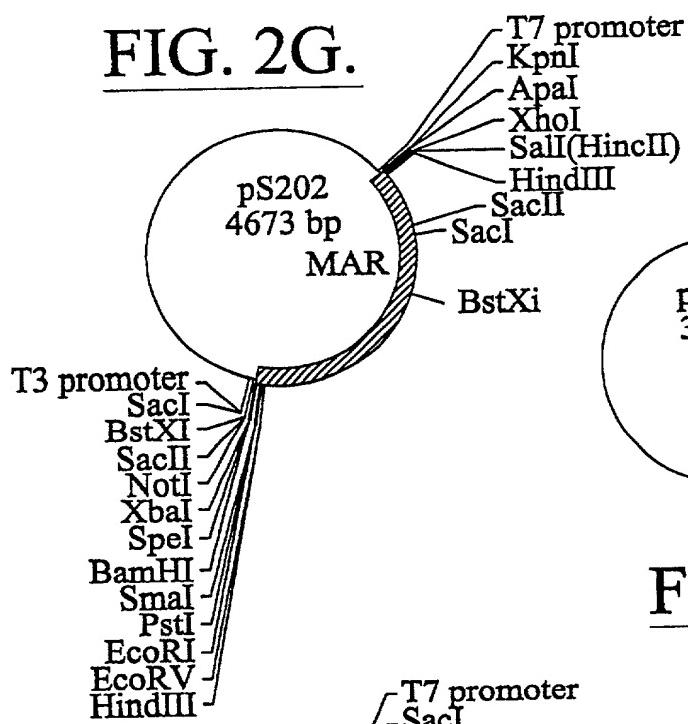


FIG. 2H.

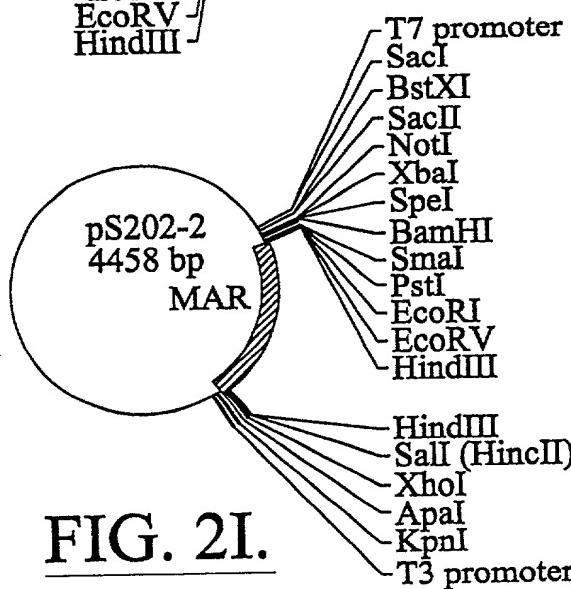


FIG. 2I.

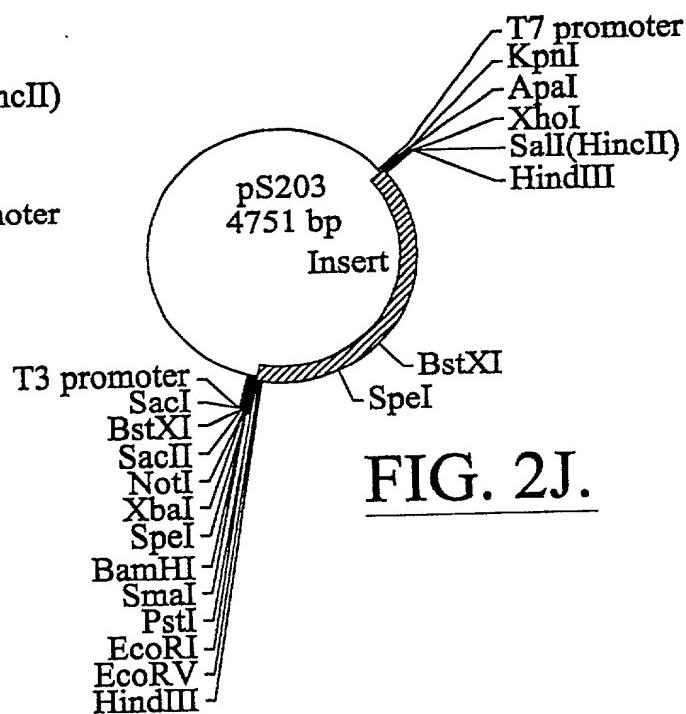


FIG. 2J.

FIG. 2K.

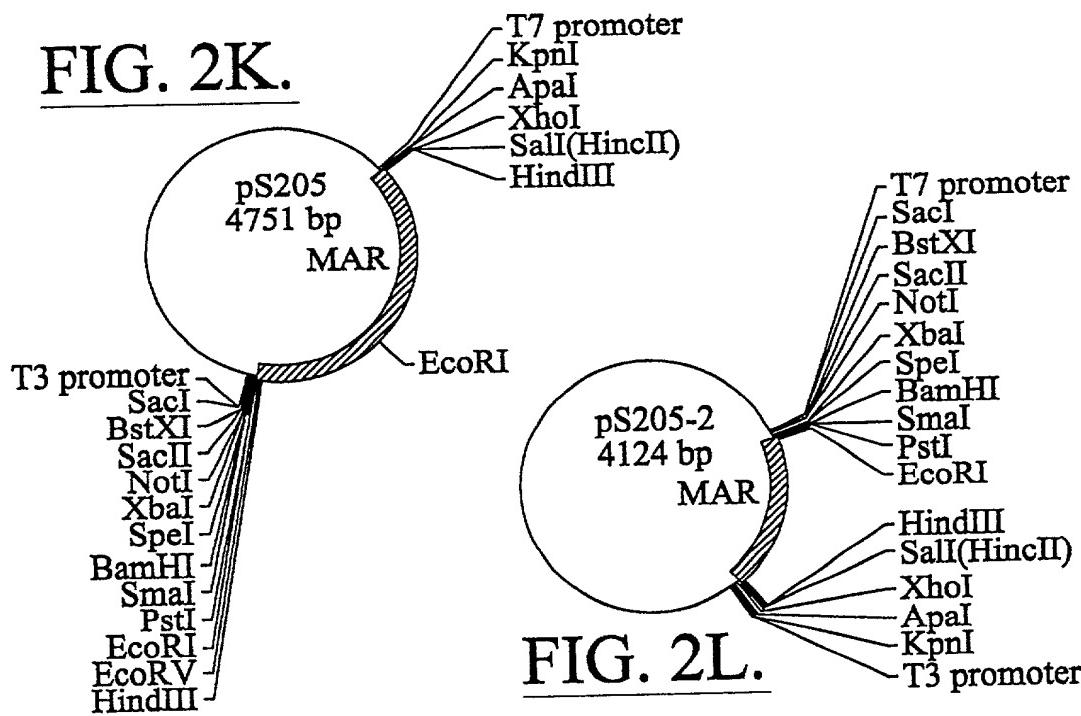


FIG. 2L.

FIG. 2M.

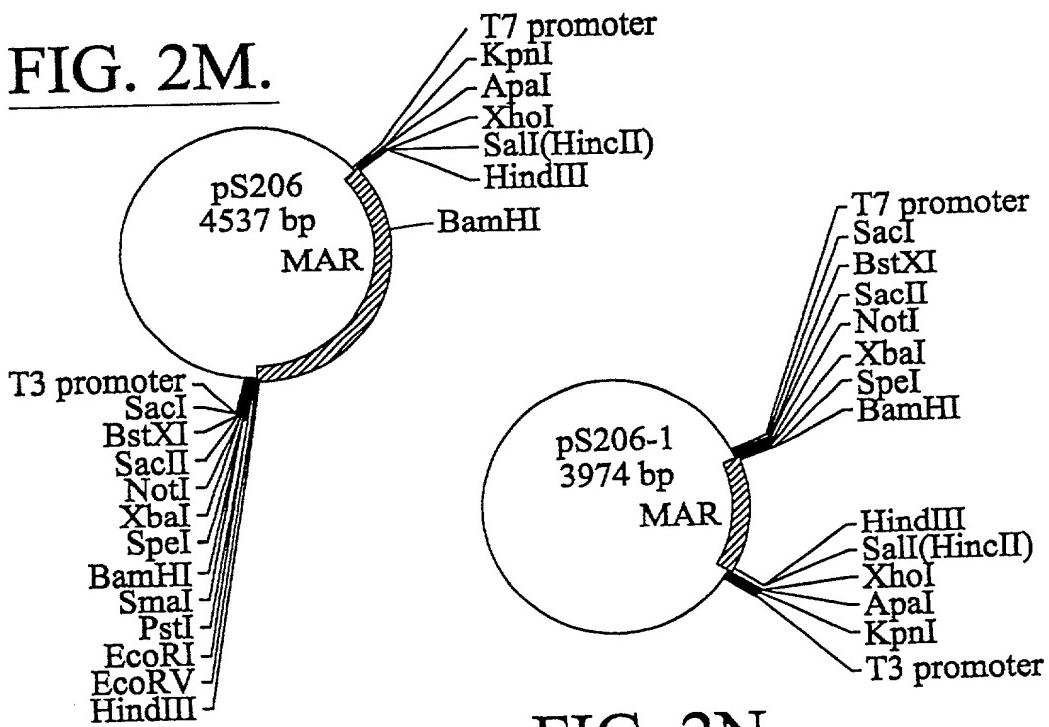


FIG. 2N.

FIG. 2O.

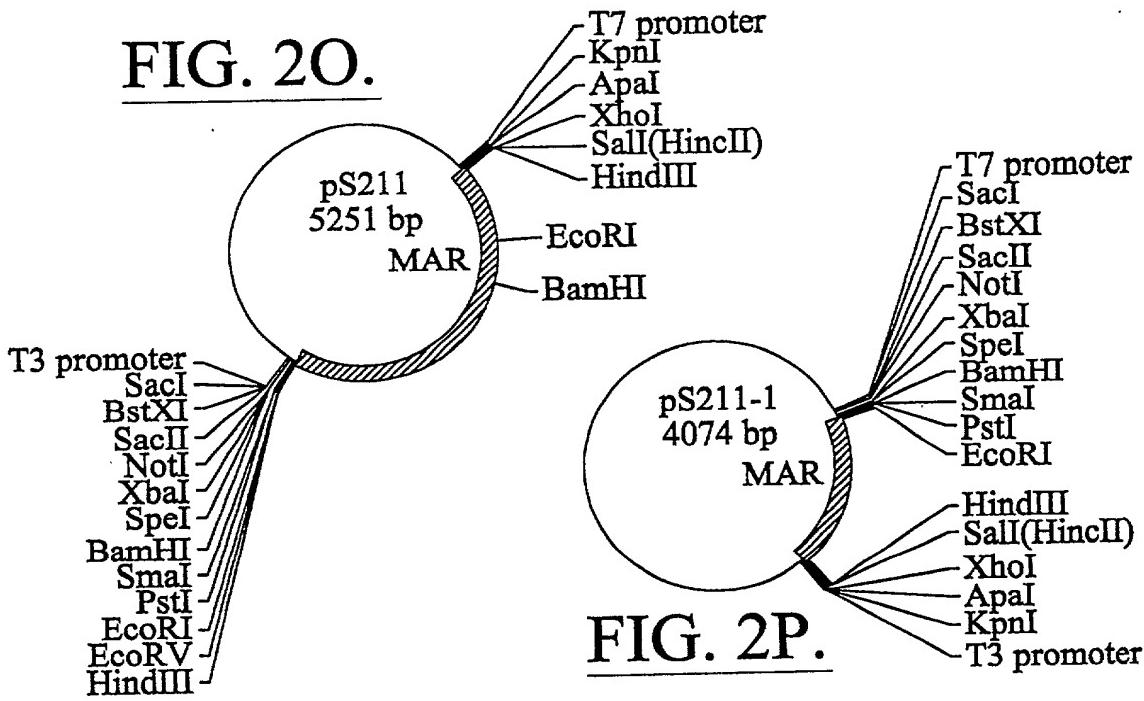


FIG. 2P.

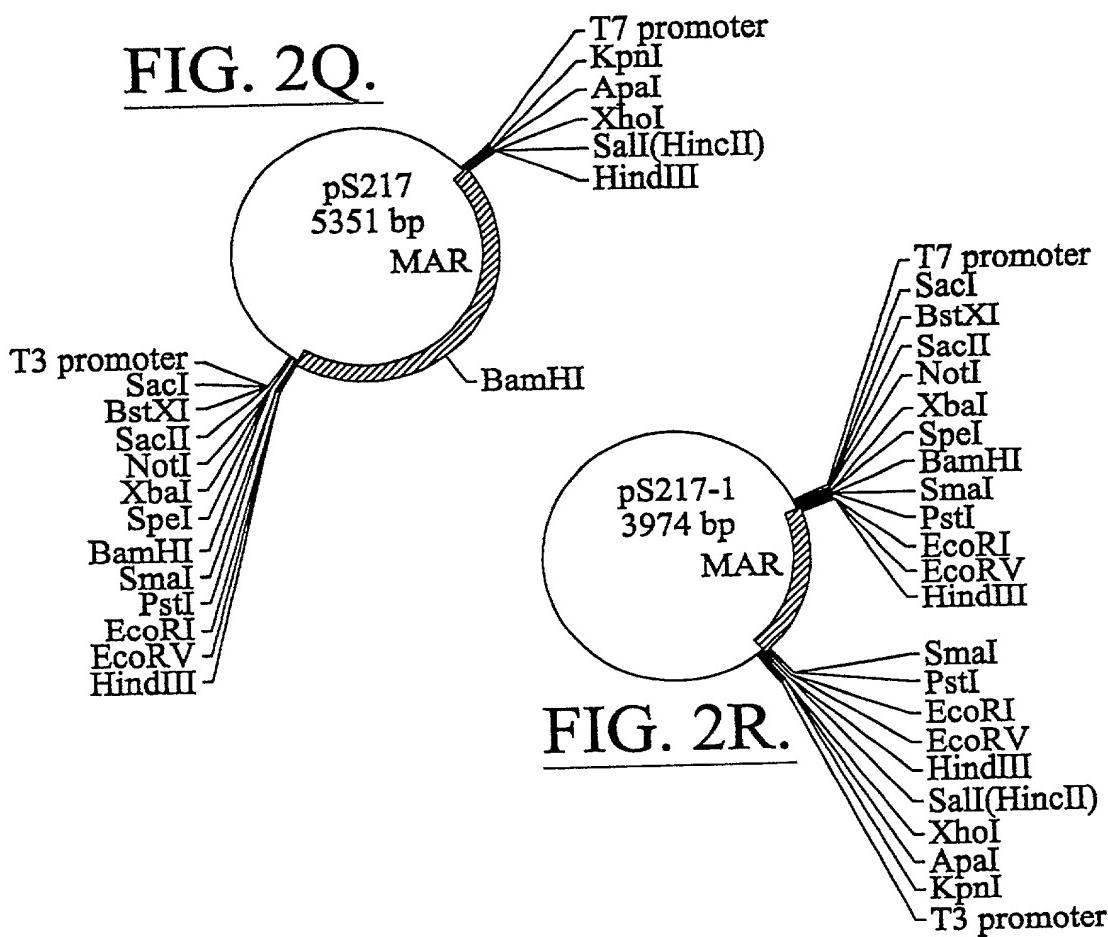


FIG. 2R.

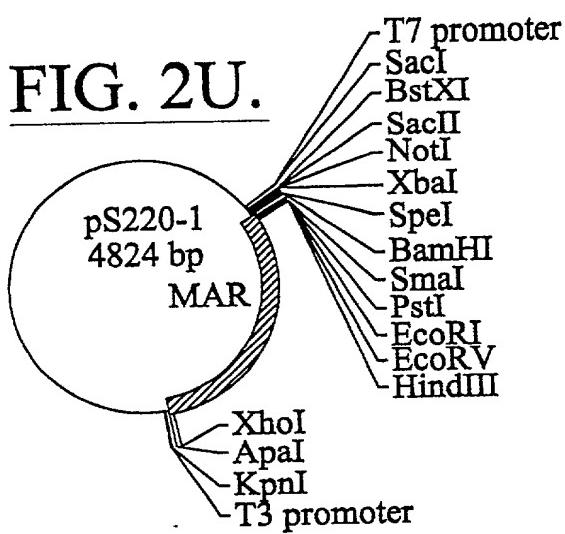
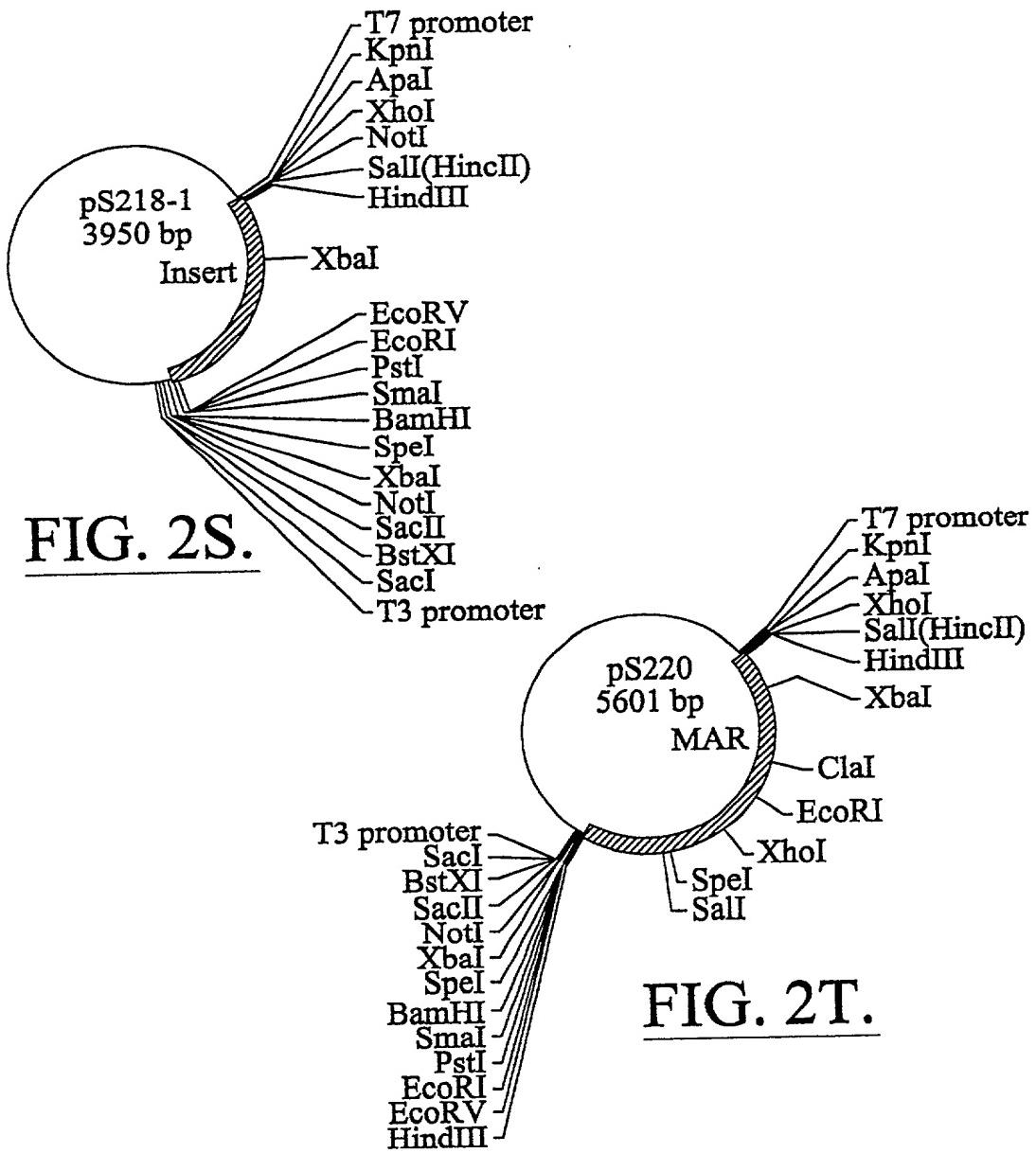


FIG. 2V.

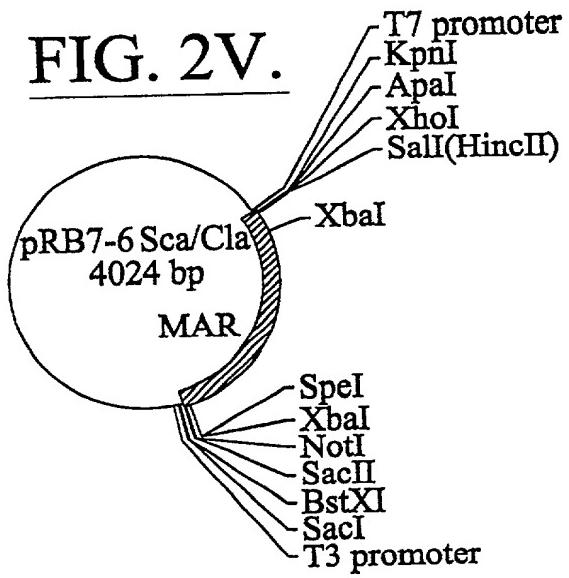
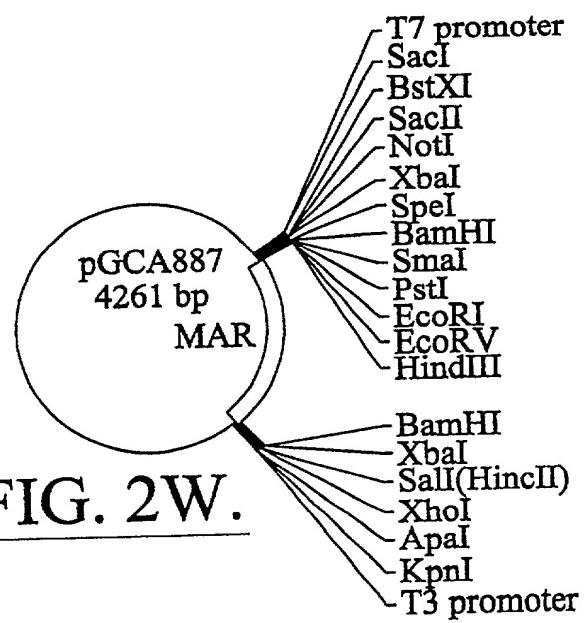


FIG. 2W.



pS1 (SEQ ID NO:1)

1 GATACTGAAA CAACGTGTAT CCAGTAAGTA TCAAGCCTAA TCTCGAAGTG
51 GTAGAGACGA GATGACCGAC TTTGACACTC ACTATGGGTC AATAATAATA
101 ACTGAAATAA AACTAAGATA TTTAAACCAA CATGATTAC AGAATTACAA
151 ATAATTTATT TAATCAGCAG AAATAATCAA ATTTCTTCAA ATGTAACAAT
201 TCTCAATATA TTAATTAAT TCCTTCATT CAAATAATT CTAATTTATC
251 AATTAAACCT CATTACAGG AGTAACAATT AATTCCCTAA CAAGCAAGAA
301 TAATAATTCA TTAAATTCCA AGGATTTTC AATTATTAA TTAGCTTCAC
351 AACCTGAAAT AAATTATTAA AGTATCGTGT AATTATTATT ATTAAGCAGC
401 ATTTCTGCCG AGGACATACG GCCCGATCCA GAGTATC

pS4 (SEQ ID NO:2)

1 GATACTAGAG TGGTGTATC AATTCTTACT CGTATGAATT AATTAAATT
51 GTCTCTTATT TCTGTCCTAA GTCATATACA AGAAATGCTA ACTCCATCCG
101 TTTCAATCCC TATGACATAG TTTGATTGAA TTGAATTGAA AAATTAAAGA
151 AACAAAAGAT AATTTTTGTG ACTCATAATT TAGACATGTG TTATAAGACT
201 TTTCTCATGA ATTTTTAGA AACAAATGAT AATTTTTGGA ACTCATAATT
251 TAGACGTTT ATAAAAAATA CTAACTGCAT CTGGTTCAAT ATTTATGTGT
301 TATTCCATAAAACTCTGG ACTTATATT TTAAATATT CATAATATT
351 GGTATCGGTA TAATTTTTGTCACTTTG GATGAAAGGG AAGTTAAC
401 AAATTCTTT TTCCAAATT AGAAAGTTAT AATATTCTTT TTAAACGCC
451 CAAAAAGAAA AATAAGCTAT TGATTATTAT AAGCCTAAC CAAAAGAATT
501 CTTTGACTAG TAGGAAGCCA TTTTTAAGTT AGGCGCCAAA ATTCAAAGCC
551 AACGTGGGCA TATCTCCAAA CTGGCGGCTA CAGTATC

pS8 (SEQ ID NO:3)

1 ACCGCTTTA TTATTATTAT TTTTACCGAG AATTACAACA TCATGAAAAT
51 ACATCTCGAA CCACGTACA TCAATGCACC CGCGGTTATT GACATATTTC
101 AACTCTGTTG AGATTGAT TTGGGTCAAA TAAATGTGCA CCCGAGTTA
151 AGAGGATAAC ATTATTAAT ACGCGCCTAA AACGACTAGC GTATCATTAT
201 TTTGGTAGG GCCGTGAAAT TTTGCTAAC TGCCCATCCA GAAATCTAAG
251 TAATTTACC AACACGTATA GAGGGCCCCA CAGCTTGTGT ATTTTGTTT
301 GTCGAGGCTC GTCTCATTCA TTATTTTAA AAGGAATTG CAACGTCGTG
351 GAAATGCATC TCGAACCAACG TCACAAATCAA TGA

FIG. 3.

pS115 (SEQ ID NO:4)

1 GAATTCGATA GACTCACTTA AATATTAGAA GTGAATTACC TAGAGTTAGA
51 TCCAAAACAA TTATCTTGCA CCTATCCTAT CAACCCCTAT CTTTCCCCT
101 TGATTACTAC CTTGCTTACCG TTTGTTACGA TTTCATTAG ACAATAACTT
151 TAGATTCTTA GTTAATTGCA GTTAGAAATT ATATTAAATT TCAATTGTTG
201 GATCATCTTG AATACCAATC AAGCTAGAAA ATACAAGAAT ACTGTTAAA
251 TCAAATCCAT GTGGATACGA TATTATACTA TATTATATTG GACTTGTGAG
301 CATTATTTAT GTGTGTTTGT TGCTCGTCAA AGTTTGGCGT CGTTGCCGAG
351 GATTGGCAAT CAATAGTGT TGAAATAGTT TTTGGTGCTA ATTTAGGAAT
401 TAGGTTTAT TTATTTATTG TTTCTTTCT TTTCTTTTC CTTTCTATT
451 TTATTCCTT TATTAGTTAA CTTCTTTCA AGATTTTTTG TGTAGTACCT
501 AACAAAGTTAG AGAAGATACT GTAGATTITG AACTCTAAAT GTTGTGAAGA
551 TGGAGTACAA CCAGCCTAAG AAAATATTG AATAGTTAGC AGCTGAACAT
601 TATCGGCGGT CGGTTATGCG GTTAAATGC GGTGGAAGCA TCTACCACCG
651 CAGCCTAAAG AAAATATTG AATAGTTAG CAGCTTGAAC ATTATCGGCG
701 GTCGGTTATG TGTTTTAAAT GCGGTGGAAA TCATCTACGG GCTAACTGTC
751 AAGCAGGTAT GTATTCTTC TATGGTTCGT ATTTGAGGA GTCTCACTCT
801 GTTTCTAGTT CGTACATGTA TGAGGATTCA TATGGGCACA ACTCTGACTC
851 TGGTTGGGAT GAATTG

pS116-1.1B (SEQ ID NO:5)

1 GAATTGTATT ATTGTTAGGT GGGAGAGATT TTTGACTATA TGGGTTAAAAA
51 TCAGCGACAA AGGGCCAAT ATACCTATTG ACTTTTAAAAA ATAGTCTAAT
101 AATACCTCTC GTTATATTAT TAGGTTATCT ATACCTTGC AGTCATATTG
151 TGGGTTCAAA TATACCCCTC ATTTAACCGG AGGGACACGT GTCATCGTCC
201 TGTTGGTCAA TTCTAAATAT CTCCTAATTA ATTAAAAAGA CTCATTACCC
251 ATATCCGAAA AATATTTTT AAAGCAATAT TTTTTATAA AAAATGGAAA
301 AACTGAAATT ATTTTACTA AAAATTGAAA AAAACGAAAA TAGTTTTTT
351 TCAGTTTTTA CAAAAAAACT ATTTAGAAA AAATTGAAAA ATATTTCTA
401 AAACAATGTT TTGTAaaaa CTGAAAAAAA AGAAGCTGAA AATCAATTG
451 CTAAAGCAAT TTATTTGTA AAATCTGGAA AAAACTACTA AAAACTGAAA
501 AAATGAAAAT ATTTTTTTTT CTAATTTTA CAAAAAAAC TGTTTAAAAA
551 AAAGCTGAAA ATATTTCTA AAACAATATT TTGTAaaaa CTAAAAAAA
601 AATATTTCT TCTTTTTTC AGTTTTAGT TAAAAATATT TAAGTTTTT
651 CCAGTTTTTA ATTACTTAG AAAATTACTT TTCTGTTTT TTTTCAGTTT
701 TTACAAAAAT ATTATTTAG AAAATATTG TCAAGTTCTT AAAGCAGTTT
751 TTTTTGTAA AAACCTGAAA ACAATATTG TCGTTTTTT CAGTTTTAG
801 TAAAATTGTT TTGTTAGTTT TTTCAGTTT TACCAAAAAT AAAATTGCTT
851 TAGAAAATTA TTTTCGGGT ATGGGTAATG GGTCTTTTA ATTAATTAGG
901 AGATATTTG AATTGATCAA TAGGACGATG ACACATGTCC CTCCGTTAA
951 ATGAGGTGTA TATTTGAATC CAAAGTAAGA CTGCAGCCCCG GGGGATCC

FIG. 3. (continued)

pS202-1 (SEQ ID NO:6)

1 GAATTCTGATA TGGCTTGTG GACAAGAATT AATGAATCAA TTGTAAAAAA
51 GTTGATGGAC ATATTGAAGG TAAAATCATA TACTATTTT CTAAAATCTC
101 TTTTAAATGT CCCCAATT A TCTGATTTCT ATATTGCTCT TAAATGTCAC
151 TCAACCTTAG ATCAACAAAC ATATAACTTA CCCAGTACAT AAGAGATTGC
201 GGCATTATGG CTTGAAGAAA ATCCTAGAGA CACATCTGCA CCACATATT
251 GAATTTATAC CCACAGTAAT AGAGCTCGGT TAGTACATTA TTATTATGGA
301 TGTTACGATC CGTTGCAGTA TCCATTATTA TTTCTTCG GTGAAAATGG
351 ATGACATTGT GGAATTAAAA AAATTATTCA GACAAAAAAT TCGACGAAAC
401 GTAGAGCTTA CTGCGAACAT GAACAATTGC CCAGTATATC AAATACGTGT
451 TCAGTTGATG GATTCTTGA TATGGAAGAT GAATCACTAC AAAGAGGAAA
501 ACGAAAAAGA GATACAGTGT CTTGTCGAGA GTATTATTGT TACAAATTTC
551 AACTAAGAAA TAATGAAACA AATGAAGTGT TACATTGTGG GAGAATATT
601 CAACAATTAA TAGTAGATAT ATATATATAA AGCTT

pS202-2 (SEQ ID NO:7)

1 AAGCTTGCAC GCCTACATCG TGGGATAATT TAGAAAAGG AAAGGGTATA
51 TTGGATCCCC CTATCATTTG TGAAACAGGT AACCATACGA GAACCCCTTT
101 CGCTTCCTGA AAAATGTTAT ATATTGTTGT ACTCATATT ATACACTATT
151 TATTATTAAT ATAACGATGC TTATTTGCT TGGAGATTGG AGATTATCAC
201 AGCTTATTAA TCTTATATTG TATCTTATTA AACTAAAAA CATAAATACT
251 ACGTGCTCTT TTAATTGGG ATCTATTAAG GGTTGTTGC ACGCTTTAA
301 ACATCTGGC TATTCTGTT ACCAGCTGCT ACCTTAGCCT GTATGCTTAC
351 ATCATCTCCT AATTAGACA AAGGAAAGGG TATATTGGAC CCCCCCTATC
401 ATTCTGAAA CAGGTAACAC TACATTAGA TTATACCTTT TTCAGAATGA
451 CATATTGTTT ATACATTACT GTAAATTGTG ACTATTGTA TATTAGGGTC
501 CACATCGGGT ACATCTAACC TGCGTCATGT TATCTTGAAC ACTGTTCAA
551 TCAAAGGTTT GCACAAACCTT AATGTTACAA TCATGTCCAC CATACTATG
601 CCTTGGTGCT CTTTTTTTC CTAATGATAC TTCTTATATA TTCAGCTCAT
651 AGGCCGGCCA GAAAGGTGTG CCTGGTCACT AAAGAGCAAC GAAGTGAGTA
701 TGTTGCTCTA AAAAGGGTCC CACACTGTCA ATTCTGTCAT CCAAAGAAGT
751 TTGAATATGA ACCTCCAGGA TTTGCTGTA ACAGTGGITC AATAAGGTTG
801 ACATCTCATA AAATGCCAAC TGAATTATCG GAGTTATACT TTGGAAATAC
851 TGAAGAATCT GAAAATTTC GAACTTATAT TAGAACATAC AATAACATGT
901 TTGCATTAC TTCACTGGT GTCAAGTATG ATAAAGAGCT AGCGAGAAGA
951 AATTGTGGTA TCTACACATT TAGAGTCCAG GGACAGATGT ATCATTAT
1001 AGATGATTAA GTTCCCTCCA ATGAAAAACC TAGGAATTAA TAGCTGTACT
1051 TCTACGATAA TGATAATGAA CTAGCCAAAT CAAGCTT

FIG. 3. (continued)

pS205-2 (SEQ ID NO:8)

1 GAATTCTTCA GCCATTGTAC ATATAGTTGT GTATTAATGT TATTAATAAT
51 GGATAATTAA ATATATACCT GGAATAAATA TACGATATTA TAATAGTGTG
101 TAATTATATA TAAAAATTAT ACATAATATA ATGATGGTAT TTAATATAGC
151 ATAATTITGA ACGATCTGGA TTGATTCTT GAATCAAAT AGAGTTGTG
201 GAAAAGAAAA GAATGAGATG AAAAGCAAAG TATGAAGAGA TGAATTGTG
251 TTTTTTTAT GGAGGGAGGA GGTTCTCAGT GATGGAATCA TCCCTGGTTT
301 TCTTAGCAC CAATGAAAGT AATGAACCCC CCCCCAAAAA AAAAAAAA
351 AAAAAAAAGG GAGAGAGAGT AGAATGGAAC GGCTAGGTGA AAGTATAGGA
401 GTAGAAATTAA GGTCAGGGA GAGAAAAGGG GGGAAATTAA TTCCTAAATT
451 AATGGGATTTC TAATTTTAA ACTGTTTGA AATATTTAA AAGTAGTGT
501 ATTATATTA TTAACTTTA AAAAAAGTC AACGAGGTAA AAATTCCATG
551 GGGGAAAATT TAAATGGTTA GTCTTCTATA ATATTTCAA CTCTGCTTAG
601 CACTAAAAT TAGTCTAAA ATAACCCTAA ATTAGTGTAT CTAATTAAAT
651 TAGTTCATCG AACAGGAGCA TTGGATTATC CCTCCAGAGT TACACAGGAA
701 GCTT

pS206-1 (SEQ ID NO:9)

1 GGATCCAGCT ATTATTATAG CATGTGAGTT GTCCGTGAAC AGCTAATTTT
51 TTACCACACC CAAATTCAAT ACTATTTAG TGAAATATA TCTTTAGGT
101 CTAGTCTAA TATTTAACCT TTTGTCCTAC TTTTAATAGA TTTTATTG
151 GAAAATTAA TAATTACAAA AAATAAAAAG TATATATTCA CATACTTATA
201 GTACAAACTT TGTTCTATT TATAAAGAGA AAAAGAAATT TTACAAAAAA
251 CAAATATATT TGCTTCTTT TAATTAGTAG TTTTATTAAG CAAGCTATAG
301 AAGCTC

pS211-1 (SEQ ID NO:10)

1 GAATTCCGTG GTTTAGCAC GGTCGCTCAA TTGTCATATT TGGCTCATT
51 ATCTGATTTT TAAACAATTAA AGAACTTATA TGCAAATTAA ACTTTTAAAA
101 CCGCTTTAT CATTATTAT TTTATACAAA ATTACAACGT CGTAAAAGG
151 CATCTCGAAC CACGCCACAA CCAGTGCACA CGTGATTGT TGACGCATT
201 TGGACTTCGT CAAGATCGTG ATTTGGTTA CATAATGTA CACCCGTAT
251 TTAAGAAAAT AACCTTATTA AATATTGCGC CAAAATACTA CGCCTTATGA
301 TACTATTAGG GTAGGCTTGT GAATTTACT AAATGCCCA TCTCGGAATC
351 TAGGTATTTT CTTATATTAA AAAAATAAG ATGGGGCCT GCAATTTTTT
401 ATTATTAAT ATTTATTAT TTTTAGCGA AGATCCCTCC CTTATTTAT
451 GAATACCCCTT TAATGACTAC ATCTTATTA TTACTAAGTT TGTCTATAAT
501 TATGAAGTCA ATCTCTACAT ACATAAAAAT AACATATTAA TTACTAATT
551 AAAACAAATA TTAATGGAAA GTAATATTAC TAAAATTATA ATTACAAACA
601 ACATGGAATT GTCACAAAAT AAAAATAAA AACTAATTAT CCCATAGTTG
651 GATTAAAATT CATATTGTTA GTATGACTTA AGCTT

FIG. 3. (continued)

pS217-1 (SEQ ID NO:11)

1 AAGCTTTAAA AGGAAGAGAG CCACAATTT CTTTGACCTT CCTTCTCTCC
51 TAGCCACTAA GATATACAGT ACTGGTCAAA AAGAGCATAT TTATAGCTCA
101 AAATTTGCC TTTTCTGTT GTAAACGTGA TTGTTTCTTA CTTGGATTCT
151 TGTTCTATAT ATTTACGGGA GAAAAGAGCA ATTTGCATGC TCCTAAATCT
201 TTTATTTCT GGTGAAAAAT TGGCTTTAA TTGGCTGGGA ATTATTTTTT
251 AGATGCTACA ACCTTGACAA ACACCTAAGA ATATTTAGT GACAATGGCT
301 TGTTCTTGA GTACTGGTT TTCTGTTCT GGTCCCTGTT TCAACGCCAC
351 AGCCAAAGAG TCTCGTCGTC ATTGCCCTTC GATTGGCACT CTGCAACTTA
401 AAGATTTAGC ATCCAGAGAA TTTCTAGGCA AACCTTGGA TTATGCATCA
451 GATCATATTG GTACTAACCA TTGGAAATGTT GAACGACTTT CTGTATGAA
501 ATCTCTGATA CATTGCTTC TGTGTTTATA CTTGGTGTTC TCATGTTTTC
551 ATTCTTGTT TAAATTTTC GAGATCAAAT CATTATAAG TATTATTCT
601 AATGATTTA GGCACAAGTA TCAATCGCTG CTCAGAGATG GTGGGAGAAG
651 ACCCTTAAAC CCAACATGGT AGAGATCAAT TCAGCAACAC AACTTGTGA
701 TTCATTATTA AAAGCTGGTA ATAGATTGGT CATAATTGAC TTCTTCTCTC
751 CTAGCTGTAG AGGTTTCAAG ACTTTACATC CTAAGGTAAG ATATATAGCA
801 ATCCCCTAAA AAAAAAAAAA AAAAAAAAAA AAACCAACAA CTACATCGTA
851 ATCCAAGCA AGTTAGGGTT AACTATATGA ATCATCACTA GACGGATCC

pS218 (SEQ ID NO:12)

1 AAGCTTAAC TTACTCACAT TGCTTTCTTT AGGGAAGCGT CTTCTTAAAT
51 GACCATCCTC TAAATTTCTC ATGAATCTTC TTCTGTTGTC CACTCTGTTA
101 TCGCTGAAAC GAAATCTGAA ATTGTCAATGA TGCTGACTAT TATCCAATCA
151 CTCAGTCTCT AATTCAATTAGATTATCT TGTTCACCAAG CCCATACTGA
201 TTTTATTGT TTTGGGGTCT AACTTTCCCT TCCGGTAGTC GGTTGGAGTC
251 ATGAACCTAT TTCTGAAAT GAGGATATGA CTTTATGGCC TATACTCTT
301 TGGTGTCTCA AGGCCTGTCA CCTCTCATCT TTTCCTTCAA TTGACTATAG
351 ACTCTGTAAT ACTGTCACTT TTGGGATCTA CCGTTGTCTT CCATGTATCA
401 TATCTTACTC ATAATGCTTC ATTAACATT TTCTTATTTC CCGCTAACAT
451 TTATGTCTAT CACTTTATTC TGAAAACCTG AACAAAGACAT TCTTTTCGTT
501 TTAGATCCCC TTTGCTCCAT CCAGTGGTTC TTCGGGGGAC TTAACGTTCT
551 CGCTCTCCTA GGGAGGCAG CCACACTAAG GTAATATTAA TCCCTTCTAG
601 GCTTCCGTG CCTATCTTCT GAGATATTAA TTTCATGCTA ATATTCACT
651 CTAATTGTAAT TTTCTAGAG TGCGCCATCT GGGTGCCTCA CAAGAAGAGC
701 TATTAGCATC TTTGTAATAT CCTTCGGAAA TGTCAACTAA CACAACACAA
751 TCCATTCACT ATTTGGGTT ACTCTAACCT CAGTCGGATA CTAATATCCT
801 GTCATTTAT TAAACTACAC ATGTTAGCCC CCAATAGGAT ATAACTAAGA
851 TGGGTGTGGC CAATTCTACA TACATCTGTT ACTGTTAAA GTAAGTCGCA
901 ATGCTTTAT TTTTCTGCCG GAGTTGAAAA TACCGATAAT CTATATTAAC
951 TGGGTACCTC GTACCCTTCT CATCTTCTC CTTTACTTG TTGAAGCTT

FIG. 3. (continued)

pS220-1 (SEQ ID NO:13)

1 AAGCTTGAAA AAGAAGAATT AAGGCTTGCT TTCTTAATT TTAAAAAAATA
51 AAAATTATTT TGAACATATCT ATACTATATT AAAAGCACGA AAACCCCTATC
101 GAAATGTCGT TCGCCTTTT TACCCTTAA AAATAATT TT ACATTAGACA
151 AAATAGTCAT TTACTATTT TTCTTAATAT ATAGGATT TT AAAATTAAATT
201 TAACCTTGCG TATTAAACAT TTCTTATAA CTTGAAATAT GTAAAACCTCC
251 TAATATTITAG AAATTTAATT AACATAACCA AGGATTTA TATCGGTAAT
301 AACTCTAATA TGGTATCCAA ATCAGTCTAG AACTCTCTA CCTCTAATAA
351 GTAAAAGTAC TTCTAATAAA TTCATATACT TTCTCTCT TCTCCGATCT
401 CTCTTGCTC TTCTTTTAT GTATCCTTTC TTCTCTAATA GCCTTTATG
451 AGAAGTAAAC TTCTAGGGTT GGCCCCCCCCT CCCCCCACAA TTATATAGTT
501 TCTTACTCAG TTGTTGGAAT ATAATTCAA TTCTTAATA ATTGACGGTG
551 ACATTGAGTT TTACTTTGTG GAAGAGAATT AGATTCTCGT GTTAGTAAAA
601 TCGGTTAGTA ATTGATGATG CATTATTTT ACTCTATAAT AGAGATGCAA
651 TTCTTATTTT GCATTTGGG ATCAAATTGT AATGCAGTCA TATATTGATT
701 TCATAAATGT TTGGGATATT GTTGGTTATT TAACTAGAAA TAGACTTCTT
751 ATTTCATATT TATTGTTAAA ATCCCTTATT GGAGATGAAT TATTGTTCA
801 CCGATTAGAA GTTGATAGTC GCTTTTGT TT TAGAAGAAAT TTTACCGTAG
851 ACCAAGTTAA GGAGTTTAG AAGCACTTTG CATGGGAGCA TTAGTGTATG
901 TTATGGCTTT ATCAAATATA GGTTTGAG ATTCAGAGAG CCAAGAAAAG
951 CTAGAACCCA AGAACTAGGA AGTTAGAGTA ATTCACAAATA CCATAACGTG
1001 ATATAAAACT TTCTTATGTA ACTCAAATCG GTAATATT TTGCTTTAGT
1051 CTTAATCGAT AAATTATTT TTATATTGA TTAGTTATAG GAGGCTCACA
1101 AAGTTGGAA TAATTAAAAT ATCATATT TT GTATTTGAAC AATTATGAA
1151 ATAGTAATTG GTAAAAAATC ACTTTAAATT TTATCCTAT ATCCAGAAGG
1201 ATTATGGTGT CTGGCATAGT TGTTTGGAAAG ATTGAATCA GGGTAAAAGT
1251 ATGTTGTAAT TTCTTATTTG TTATAGGCAT TTGCTTGCT TGATTGTTT
1301 GTTGTCTTA TATTTTATTA TTGGGAAGTG TATATATATG TTGATTAAA
1351 ATATAGATAA TCAATTAT AAGAAATTG CAACAATTAC ACAAGGATAA
1401 AGCTACAAT ATGCGAGTAA AATTGATTG AACCTAGGAT GTCATATT
1451 ATGCATATT TATTCAATG TGTTTATTAT ACATCTATTG TATTATATG

FIG. 3. (continued)

CLONE	%AT	BINDING STRENGTH	GRAPHIC REPRESENTATION
pS116-1	76.6		
(SEQ ID NO: 5)			
	90		<p>Sequence: UU U UUUUROU T T ATA TAT AT T TA A TATT AT AATA U OU UUUUUU</p>
RB7-6	73.2		
(SEQ ID NO: 20)			
	80		<p>UORR R U UU AT AA AA A AT AAA O A T TA U T TA U U O O T U</p>
pS211-1	71.7		
(SEQ ID NO: 10)			
	70		<p>T OR O TATTAA A A T TAA ATT R O O R</p>
pS220-1	73.1		
(SEQ ID NO: 13)			
	70		<p>A AT AAAA U T R U AT A A A AAAAA O R R R AAT AA R A</p>
pS226-1	77.1		
(SEQ ID NO: 9)			
	60		<p>UUO U AA A U TATA U R U</p>
pS205-2	71.4		
(SEQ ID NO: 8)			
	50		<p>AAA R R T AA A TT A OOUR U R A TA A TT A</p>
Ps217-1	65.2		
(SEQ ID NO: 11)			
	40		<p>OU RR TT T AAA AAAA AA A TT</p>

FIG. 4.

<u>CLONE</u>	<u>%A+T</u>	<u>BINDING STRENGTH</u>	<u>GRAPHIC REPRESENTATION</u>
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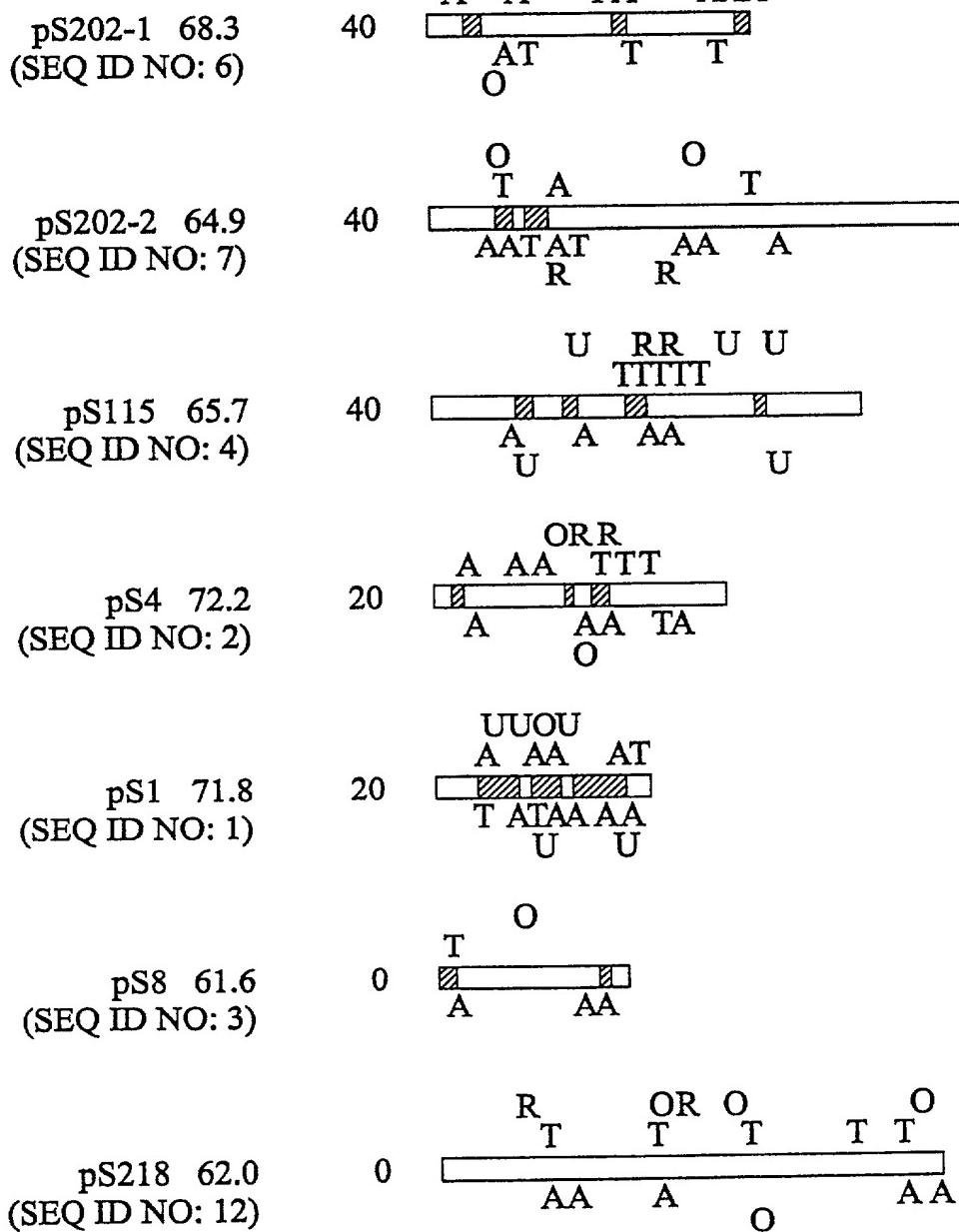


FIG. 4A.

